

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 31, 2003, 13:28:52 ; Search time 41 seconds
(without alignments)
1233.774 Million cell updates/sec

Title: US-10-082-894-2

Perfect score: 2786

Sequence: 1 MDKYQNVQKVCVLWIDGWS.....LMGLPVPEMDGVPLLEQRG 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1900 | 68.2 | 539 | 2 T32749 | hypothetical prote |
| 2 | 1143.5 | 41.0 | 510 | 2 A11750 | phosphoglycerate m |
| 3 | 1141.5 | 41.0 | 510 | 2 AH1381 | phosphoglycerate m |
| 4 | 1127 | 40.5 | 511 | 2 T46885 | phosphoglycerate m |
| 5 | 1120 | 40.2 | 510 | 2 E84094 | 2,3-bisphosphoglyc |
| 6 | 1118 | 40.1 | 511 | 2 D69675 | phosphoglycerate m |
| 7 | 1088.5 | 39.1 | 515 | 2 G83004 | phosphoglycerate m |
| 8 | 1083.5 | 38.9 | 510 | 2 G82335 | phosphoglycerate m |
| 9 | 1081 | 38.8 | 507 | 2 AF0974 | phosphoglycerate m |
| 10 | 1078 | 38.7 | 533 | 2 AG2328 | 2,3-bisphosphoglyc |
| 11 | 1073.5 | 38.5 | 515 | 2 AH0008 | phosphoglycerate m |
| 12 | 1065 | 38.2 | 510 | 2 F96987 | 2,3-bisphosphoglyc |
| 13 | 1063 | 38.2 | 514 | 2 S47833 | probable phosphogl |
| 14 | 1059 | 38.0 | 514 | 2 B91190 | hypothetical prote |
| 15 | 1059 | 38.0 | 514 | 2 C86037 | hypothetical prote |
| 16 | 1055 | 37.9 | 510 | 2 A56142 | phosphoglycerate m |
| 17 | 1023 | 36.7 | 508 | 2 S73540 | phosphoglycerate m |
| 18 | 1023 | 36.7 | 532 | 2 S76482 | probable phosphogl |
| 19 | 999.5 | 35.9 | 505 | 2 AD2983 | hypothetical prote |
| 20 | 999.5 | 35.9 | 505 | 2 C98300 | hypothetical prote |
| 21 | 996 | 35.8 | 491 | 2 F64641 | probable phosphogl |
| 22 | 991 | 35.6 | 491 | 2 G71872 | 2,3-bisphosphoglyc |
| 23 | 990.5 | 35.6 | 534 | 2 S73300 | phosphoglycerate m |
| 24 | 975 | 35.0 | 505 | 2 H89850 | hypothetical prote |
| 25 | 967.5 | 34.7 | 508 | 2 G84339 | phosphoglycerate m |
| 26 | 961.5 | 34.5 | 510 | 2 S42705 | probable phosphogl |
| 27 | 955.5 | 34.3 | 507 | 2 E64277 | phosphoglycerate m |
| 28 | 894.5 | 32.1 | 492 | 2 H81387 | phosphoglycerate m |
| 29 | 844.5 | 30.3 | 505 | 2 C90569 | hypothetical prote |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 739 | 26.5 | 559 | 2 S44373 | phosphoglycerate m |
| 31 | 726 | 26.1 | 559 | 2 S60473 | phosphoglycerate m |
| 32 | 721 | 25.9 | 556 | 2 S49647 | phosphoglycerate m |
| 33 | 720 | 25.8 | 559 | 2 A42807 | phosphoglycerate m |
| 34 | 699.5 | 25.1 | 502 | 2 A82925 | phosphoglycerate m |
| 35 | 687 | 24.7 | 575 | 2 G86231 | hypothetical prote |
| 36 | 608.5 | 21.8 | 488 | 2 T09138 | phosphoglycerate m |
| 37 | 581.5 | 20.9 | 232 | 2 PQ0538 | probable phosphogl |
| 38 | 341.5 | 12.3 | 182 | 2 S77784 | probable phosphogl |
| 39 | 136.5 | 4.9 | 414 | 2 B90186 | phosphonopyruvate |
| 40 | 121 | 4.3 | 410 | 2 E75190 | probable phosphono |
| 41 | 119 | 4.3 | 430 | 2 T21060 | hypothetical prote |
| 42 | 111.5 | 4.0 | 545 | 2 E82074 | crp synthase VC244 |
| 43 | 110 | 3.9 | 709 | 2 T16584 | hypothetical prote |
| 44 | 110 | 3.9 | 880 | 2 T02245 | hypothetical prote |
| 45 | 109 | 3.9 | 412 | 2 B71222 | probable phosphono |

ALIGNMENTS

RESULT 1

T32749

hypothetical protein F57B10.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000

C:Accession: T32749

R:Greco, T.; Elliott, G.; Keppler, D.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid F57B10.

A:Reference number: Z21219

A:Accession: T32749

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-539 <GRE>

A:Cross-references: EMBL:AF039713; PIDN:AAE96720.1; GSPDB:GN00019; CESP:F57B10.3

A:Experimental source: strain Bristol N2; clone F57B10

C:Genetics:

A:Gene: CESP:F57B10.3

A:Map position: 1

A:Introns: 18/1; 64/1; 115/3; 151/1; 200/2; 242/3; 387/3; 503/3

C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

| | | | | |
|-----------------------|--------|--|--------|----------------|
| Query Match | 68.2% | Score 1900; | DB 2; | Length 539; |
| Best Local Similarity | 66.7%; | Pred. No. 6.6e-145; | | |
| Matches | 352; | Conservative | 76; | Mismatches 86; |
| | | | Indels | 14; |
| | | | Gaps | 5; |
| Qy | 1 | MDKYQNVQKVCVLWIDGWSDEQHGNATIAKATPIMDKLCSGNWOKLEAHGLHVLGPE | 60 | |
| Db | 21 | MANNSSVANKVCVLWIDGWSDEDPYGNAILNAQTPVMDKLCSGNWAQIEAHGLHVLGPE | 80 | |
| Qy | 61 | GLMGNSEVGHNLICAGRVIVQDIVRINLAVQNEFVNTPQIVASAEAKKSGRLHLGL | 120 | |
| Db | 81 | GLMGNSEVGHNLICAGRVIVQDIVRINLAVKNNKFNVTNLSLVDRACDRKNGRLHLAGL | 140 | |
| Qy | 121 | VSDGCVSHSHDHPALIRAKFKQLQKPVKFIFHFDAGDRDTSPTSGAGVLEQLQFIASEK- | 179 | |
| Db | 141 | VSDGCVSHSHDHPALIRAKFKQLQKPVKFIFHFDAGDRDTSPTSGAGVLEQLQFIASEK- | 198 | |
| Qy | 180 | --YGEIATITGRYYAMDNRKRWIRKMAEYAIIVGIGOKATVDAKDVVRRYRQAQSEDE | 237 | |
| Db | 199 | TYGKGLATVGRYYAMDNRKRWIRKMAEYAIIVGIGOKATVDAKDVVRRYRQAQSEDE | 258 | |
| Qy | 238 | FLKPIFV-SDDGRVKDDDTLFFNFRADRMQICEGLGLERYKDLNSVPPKNIQSGM | 296 | |
| Db | 259 | FLKPIIILQEGKRVQNDDTIIFDYRADRMREISAAAMGMDRYKDCNSKLAHPSNLQVYGM | 318 | |
| Qy | 297 | TOYNKEFPFLSPFPVTHNVLAELASQGVTFQHCATEKYKYPHVTFFNGREVFQODE | 356 | |
| Db | 319 | TOYKAEFPFLSPFPVTHNVLAELASQGVTFQHCATEKYKYPHVTFFNGREVFQODE | 378 | |
| Qy | 357 | ERCMVPSKPEVATYDLKPEMNAAGVAEKMYEQIESGRHPLVMCMFAPDMVGHGTFKPEPA | 416 | |

Db 474 -----GVTLEGGGR-LADVAPTMDLLGLGVKKPAEMTGESLIQK 510

RESULT 3
AH1381
phosphoglycerate mutase homolog pgm [imported] - Listeria monocytogenes (strain EGD
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1381
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blo-
.: Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsih,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueño, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weh-
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1381
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-510 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00534.1; PID:g16411944; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: pgm
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

| | Query Match | 41.08; | Score 1141.5; | DB 2; | Length 510; |
|----|-----------------------|---|--------------------|-----------------|--------------------|
| | Best Local Similarity | 44.08; | Pred. No. 7.7e-84; | | |
| | Matches 230; | Conservative | 92; | Mismatches 174; | Indels 27; Gaps 7; |
| Qy | 11 | VCLVVIDGWLSDBOHGNATAKAKTPTMDKLCGNWQ-----KLEAHGLHWGLPEGLMGN | 65 | | |
| Db | 6 | VAILLDGFKRAETGVNAQAANKPNDRY----WADFPHELKAAGLDVGLPEGGQGN | 61 | | |
| Qy | 66 | SEVGHNLNAGRIYQDVRINLAVORNEEFTNPQIVASAEARAKGSRGLHLGLVSDGG | 125 | | |
| Db | 62 | SEVGHNTNAGRIYQSLTRIDKAIEBGEFQENKALNAFTHTKENNSDLHLFLLSDGG | 121 | | |
| Qy | 126 | VHSHIDLFLALTRAKQLQVPKVIHFADGROTSPTSGAGYLEBOLLQFTASEKYGELAT | 185 | | |
| Db | 122 | VHSHINHLVALLETAKDKGVKNYVIAFLDGRDVAPOSSLEYLETQKATSDLNYGAIAT | 181 | | |
| Qy | 186 | ITGRYAMDRDKWERIKMAYEAIVGGIGQKATVDKADVVRERYAQSDEFLKPIVFS | 245 | | |
| Db | 182 | VSGRFYAMDRDKWEREKAYKALVSAGEK--FEDFIELVKASYANDKNEFVVPAILT | 239 | | |
| Qy | 246 | DGCR-----VKDDDTLIFNFYRADRMRIQCECLGLERYKDLNSSVPHPKNTQISGMTQYNK | 301 | | |
| Db | 240 | KDGKPVATVKDNDVAFENFRPDRAIQLSNFATDKEMDHFDRGADHPKNIKFTVMTLYNP | 299 | | |
| Qy | 302 | EFFPSPFLPPVTHTNVLAEWLASQGVTFQHCATEKYPHYVTFEFGGREGVQFQDEERCW | 361 | | |
| Db | 300 | SIDAEVAFEPIMKNVIGELNSQLSRLAETEKYPHYVTFEFGGREGVQFQDEERCW | 359 | | |
| Qy | 362 | PSKEVATYDLKPEMNAAGVAEKVMEQIESGRPLVMCNFAPPDMVGHGTCKFEPVAKQC | 421 | | |
| Db | 360 | NSPK-VETYDLQPEMSAYETDALVEDIKNDKDAIILNFANPDWVGHSGMLETIKAE | 418 | | |
| Qy | 422 | ATDEAIKIFEACQTYNVILMVTSDHGNAKMIAPDGSHTAHCNIVPFTCSKSTVFVK | 481 | | |
| Db | 419 | AVDENLGRVVDLILEKGSAAIFADHGNSETMTSGPKPHTATTVPVPVIVTKK----- | 473 | | |
| Qy | 482 | STPPTGDGGERARALRDVAPTVLQMLGLVPPEMDGVPLLEQ | 524 | | |
| Db | 474 | -----GVTLEGGGR-LADVAPTMDLLGLGVKKPAEMTGESLIQK 510 | | | |

RESULT 4
T46865
phosphoglycerate mutase (EC 5.4.2.1), 2,3-diphosphoglycerate-independent [validate=] C:Species: Bacillus stearothermophilus
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 18-Aug-2000

RESULT 4
T46865
phosphoglycerate mutase (EC 5.4.2.1), 2,3-diphosphoglycerate-independent [validate=]
C:Species: *Bacillus stearothermophilus*
C:Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text change 18-Aug-2000

C:Accession: T46865
R:Chander, M.; Setlow, P.; Lamani, E.; Jedrzejewski, M.J.
submitted to the EMBL Data Library, January 1999
A:Description: Structural studies on a 2,3-diphosphoglycerate independent phosphoglycerate kinase from *Bacillus halodurans*
A:Reference number: 224112
A:Accession: T46865
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-511 <CH>
A:Cross-references: EMBL:AF120091; PIDN:AAD26328.1
C:Genetics:
C:Function:
A:Note: cofactor Mn(2+) absolute and specific requirement; catalyzes the transfer of a phosphate group from 2,3-bisphosphoglycerate to a protein
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
C:Keywords: intramolecular transferase; isomerase; manganese

Query Match 40.5%; Score 1127; DB 2; Length 511;
Best Local Similarity 42.7%; Pred. No. 1.1e-82;
Matches 224; Conservative 104; Mismatches 169; Indels 28; Gaps 8;

QY 8 QOKVCLVVDGGLSDEQHGNAIAKAKTPIMDKLCSGNWQ-----LEAHGLHVLGPGL 62
DB 3 KKPVALIILDGFALRDYGNVAVNAQANKPNFDY----WNEYPHTTLKACGEAVGLPEQ 58
QY 63 MGNSEVGHNLGAGRVYQDVRINLAVORNEFTVNPQIVASAEAKKSGSLHLLGLVS 122
DB 59 MGNSEVGHNLGAGRVYQSLTRINLAVORNEFTVNPQIVASAEAKKSGSLHLLGLVS 118
QY 123 DGGVHSHIDHLPALIRAFKQLQVQKVIHFFADGRDTSPTSGAGYLEQLLOFIASEKYE 182
DB 119 DGGVHSHIDHLPALIRAFKQLQVQKVIHFFADGRDTSPTSGAGYLEQLLOFIASEKYE 178
QY 183 LATIGRYAMDRDRKWRERIKMAYEAVIGGICQKATVDKAVDVVRERVAQSTDFELKP- 241
DB 179 IATLGRYVMDRDRKWRERIKMAYEAVIGGICQKATVDKAVDVVRERVAQSTDFELKP- 236
QY 242 IVFSDGGR---VKDDDTLIFNRYADRMROICELGLERYKDLNLSVPHKNIQISGMT 297
DB 237 VIVREGRPVATIQNDALIFNRPDRAIQISNTFTNDFREFDGRGPKHPLFVCLT 296
QY 298 QYKKEFPFPFPPTHTNVLAEWLSQVTFHCAETEKYPHVTFHFFGREGVQFQDEE 357
DB 297 HESVTVGVYVAFKPTNLDNTIGEVLSQHLRLQRIAEETEKYPHVTFHFFGREGVQFQDEE 356
QY 358 RCWVSPKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPPDMVGHGTGFEPVAV 417
DB 357 RILINSRK-VPTYDLKPEMSAYEVDALLKEADKDYAILNLYANPDVGVHSGKLEPTI 415
QY 418 KACQATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAPDGSSEHTAHTCNLPVFTCSKT 477
DB 416 KAVEAVDECLGKRVDAILAKGGIAITADHNADEVLTDPGKPPQAHATTNPVPIVTRKG 475
QY 478 VFYKSTPTTGGDKERARARADVAPTQLQMLGPPVPPMDGVPLLE 522
DB 476 IKLR-----DGG-----ILGLDAPTMDDLLGLPQPKEMTGKSLI 509

RESULT 5
E84094
2,3-bisphosphoglycerate-independent phosphoglycerate mutase pgm [imported] - Bacillus ha
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
R:Accession: E84094
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E84094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-510 <STO>

A:Cross-references: GB:AP001519; GB:BA000604; NID:gi0176109; PIDN:BA07276.1; GSPD3:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: pgm
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 40.2%; Score 1120; DB 2; Length 510;
Best Local Similarity 43.0%; Pred. No. 4.2e-82;
Matches 226; Conservative 98; Mismatches 174; Indels 28; Gaps 8;

QY 8 QOKVCLVVDGGLSDEQHGNAIAKAKTPIMDKLCSGNWQ-----LEAHGLHVLGPGL 62
DB 3 KKPVALIILDGFAMRDEAGNAVNAQANKPNFDY----WNOYPHALLKADGEAVGLPEQ 58
QY 63 MGNSEVGHNLGAGRVYQDVRINLAVORNEFTVNPQIVASAEAKKSGSLHLLGLVS 122
DB 59 MGNSEVGHNLGAGRVYQSLTRVNLISREGFEFFENETFLNMMNHVKKSGSLHLLGLVS 118
QY 123 DGGVHSHIDHLPALIRAFKQLQVQKVIHFFADGRDTSPTSGAGYLEQLLOFIASEKYE 182
DB 119 DGGVHSHIDHLPALIRAFKQLQVQKVIHFFADGRDTSPTSGAGYLEQLLOFIASEKYE 178
QY 183 LATIGRYAMDRDRKWRERIKMAYEAVIGGICQKATVDKAVDVVRERVAQSTDFELKP- 241
DB 179 LATLGRYAMDRDRKWRERIKMAYEAVIGGICQKATVDKAVDVVRERVAQSTDFELKP- 236
QY 242 IVFSDGGR---RVKDDDTLIFNRYADRMROICELGLERYKDLNLSVPHKNIQISGMT 297
DB 237 VITNEDGSPVATIEDDAIIFNRPDRAIQMSQVFTNKRDFGRGKLPONVYVCLT 296
QY 298 QYKKEFPFPFPPTHTNVLAEWLSQVTFHCAETEKYPHVTFHFFGREGVQFQDEE 357
DB 297 HESVTVGVYVAFKPTNLDNTIGEVLSQHLRLQRIAEETEKYPHVTFHFFGREGVQFQDEE 356
QY 358 RCWVSPKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPPDMVGHGTGFEPVAV 417
DB 357 RILINSRK-VATYDLKPEMSAYEVDALLNEADKHDVILNLFANPDVGVHSGMGLPTI 415
QY 418 KACQATDEAIGKIFACQTYNVLMVTSDHGNAEKMIAPDGSSEHTAHTCNLPVFTCSKT 477
DB 416 KAVEAVDECLGKRVDAILAKGGAAVITADHNADEVLTLEGAPMTAHTNKVPVIVTEBG 475
QY 478 VFYKSTPTTGGDKERARARADVAPTQLQMLGPPVPPMDGVPLLE 523
DB 476 LNLR-----EDG-----ILADLSTPTVLDLGLGKQPAEMTGKTLIK 510

RESULT 6
D69675
phosphoglycerate mutase (EC 5.4.2.1), 2,3-diphosphoglycerate-independent [validated]
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
R:Accession: D69675; 140024
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabbet, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portez
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Se
keuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiwa
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69675
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-511 <KUN>

A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15396.1; PID:g2635904
A:Experimental source: strain 168
R:Leyva-Vazquez, M.A.; Setlow, P.
J. Bacteriol. 176, 3903-3910, 1994
A:Title: Cloning and nucleotide sequences of the genes encoding triose phosphate isomerase
A:Reference number: 140022; MUID:94292408; PMID:80211172
A:Accession: I40024
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-232, 'C', 234-431, 'MV', 434-444, 'D', 446-511 <RES>
A:Cross-references: GB:L29475; NID:g460256; PIDN:AA21680.1; PID:g460258
C:Genetics:
A:Gene: pgm
C:Function:
A:Description: EC 5.4.2.1 [validated, MUID:94292408]
A:Note: 2,3-bisphosphoglycerate-independent but M2+2-dependent enzyme [validated, MUID:94292408]
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
C:Keywords: intramolecular transferase; isomerase

Query Match 40.1%; Score 1118; DB 2; Length 511;
Best Local Similarity 42.7%; Pred. No. 6.1e-82;
Matches 225; Conservative 99; Mismatches 175; Indels 28; Gaps 6;

QY 8 QQKVLVVDGSLSDQHGNAIAKAKTPIMDKLCSGNW-----QKLEAHLHVLPEGL 62
Db 3 KPAALILDFGLRNETVGNVALAKKPNFDY---WNOYPHOTLTASGEAVLPEQ 58
QY 63 MGNSEVGHNLGAGRIYQIDVRINLAVORNEFTNPQIVASERAKKGGGRHLGLVLS 122
Db 59 MGNSEVGHNLGAGRIYQSLTRVNVAREGERFERNQTFDLAISNAKENKALHLGLLS 118
QY 123 DGGVSHIDLHLFAIRAFKOLQVQVFIHFADGRDTSPTSGAGYLEQLQFIASEKYGE 182
Db 119 DGGVSHSHNLHALLAKKEGLTKVYIHGFLGRDVGVPQTAKTYINQLNDQIKEIGVGE 178
QY 183 LATITGRYYAMDRKWERIKMAYEALVGGIGQKATVDKADVVRERYAQSEDFLKP 242
Db 179 IASIGRYYSMDRKWRVEKAYRAMAYGEG--PSYRSALVDVDSYANGIYDFEVPIS 236
QY 243 VFSDD-----GRVKDDDTLFFNYRADRMQICEGLERYKDLNSSLVPHPKNIQISGMT 297
Db 237 VITKENGEPVAKIQDGSVIFYNFRPDRAIQISNTNDRDFRDGENYKPNLYFVCLT 296
QY 298 QYNKEFPFSLPPVTHNVLAELWLASQGVTFPHCAETEKYPHVTFEFGNGREVQFQDEE 357
Db 297 HFSETVDGYVAFKPINLNTVGEVLVSHQGLKQLRIAEETEKYPHVTFEFGNGREVQFQDEE 356
QY 358 RCMVPSKPEVATYDLAPENNAAGVAKMVEQIESGRHPLVMCNFAPPDMVGHGTFKPEAV 417
Db 357 RLILNSPK-VATYDLAPENSAEYVKDALVKEIDAKHDAILNANPDVWGHSGWVEPTI 415
QY 418 KACQATDEAIGKTFEACQYNYVLMVTSDHGNAEKMAPDGSSEHTAHTCNLVPTCSST 477
Db 416 KAJEAVDECLGEVVDAILAKGHAIIITADHGNADILITESGEPTAHTNPVPVITKEG 475
QY 478 FVEKSTPPGDDGKERARALRDVAPTVLQMLGLPVPPEMDGVPPLLEQ 524
Db 476 ITLR-----EGGILGDLAPTLLDGLGVEKPEKMTGSLIOK 511

RESULT 7
G83004
Phosphoglycerate mutase PA5131 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83004
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83004

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <STO>
A:Cross-references: GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AA08516.1; GSPDB: N
A:Experimental source: strain PA01
C:Genetics:
A:Gene: pgm; PA5131
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 39.1%; Score 1088.5; DB 2; Length 515;
Best Local Similarity 45.0%; Pred. No. 1.5e-79;
Matches 232; Conservative 78; Mismatches 180; Indels 25; Gaps 9;

QY 13 LVVIDGWSLSDQHGNAIAKAKTPIMDKLCSGNWKL-EAHGLHVLHVLPEGLMGNSEVGH 71
Db 10 LIILDFGHSSEPDYNAIYAAKPVWDRLLATOPHGLISGSGMDVGLPDQMGSEVGHM 69
QY 72 NTGAGRVIVODIVRINLAVORNEFTNPQIVASERAKKGGGRHLHGLVSDGSGVSHID 131
Db 70 NLGAGRVVYQDFTRVTKAIRIDGFEFFENVIAGAVDKAADAADKAVHILGLLSPGVSHED 129
QY 132 HLFALIRAFKOLQVQVFIHFADGRDTSPTSGAGYLEQLQFIASEKYGELATITGRY 191
Db 130 HLVAQMAARRGAGKIYILHFLDGRDTPPKSAQPSLERLDATFAGLGKRIASIIIGRYF 189
QY 192 ANDRDKRWIRIKMAYEALVGGIGQKATVDKADVVRERYAQSEDFLKPPIVFSDDG--- 248
Db 190 ANDRDNRWDRVQAAYELIVDGKAE-FTADSSVAALAAAYARGESDEFVATATVPAGAEA 248
QY 249 -RVKDDDTLFFNYRADRMQICEGLERYKDLNSSLVPHPKNIQISG---MTQYKNEPP 304
Db 249 VRVEDGDAVIFNFRADRAELSRFAVEPAFNEF---PRERAPOLAGVFLMTQYAASTP 304
QY 305 FFSRLPPVTHNVLAELWLASQGVTFPHCAETEKYPHVTFEFGNGREVQFQDEERCMVPS 364
Db 305 ACAPFPPELTVNLVGLYLAHKGTKQRIAEETEKYPHVTFEFGNGREVQFQDEERCMVPS 364
QY 365 KEVATYDLAPENNAAGVAKMVEQIESGRHPLVMCNFAPPDMVGHGTFKPEAVKACQATD 424
Db 365 K-VATYDLQPENSAPEVTDRIEAEIQQYDVIVVYANGDMVGHGTFEFAAVKAVECLD 423
QY 425 EAIGKTFEACQYNYVLMVTSDHGNAEKM-IAPDGESEHTAHTCNLVPTCSSTFTVFKST 483
Db 424 TCMGRIVEALDKVGGESALITADHGNVEQMEDESTGQAHTAHTCEPVPF-----VYVGKRR 478
QY 484 PPTGDDGKERARALRDVAPTVLQMLGLPVPPEMDG 518
Db 479 LSIREGG-----VLADVAPTMLTLMGLEQPAEMTG 508

RESULT 8
G82335
phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent VC0336 [imported] - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: G82335
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellens, L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: G82335
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-510 <HEI>
A:Cross-references: GB:AE004122; GB:AE003852; NID:g9654745; PIDN:AAF93509.1; GSPDB:3N
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0336
A:Map position: 1
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 38.9%; Score 1083.5; DB 2; Length 510;
Best Local Similarity 43.1%; Pred. No. 3.6e-79;
Matches 226; Conservative 87; Mismatches 180; Indels 31; Gaps 10;

QY 6 NVQKVCVAVIDGWSLDSQHGNAIAKAKTPTIMDKLCSGNWOKL-EAHGLHVLPLGSLMG 64
DB 2 SAAKPHALVLDGWSYREDNANNAINNARTPYMDSLMANNPTLISASGMDVGLPDQMG 61
QY 65 NSEVGHNLICAGRIYVQDITVRINLVAQRNEFTNPQIVASAEAKKGSRLHLGLLVSDG 124
DB 62 NSEVGHNLICAGRIYVQDITRITKATMDGEFOHKNVLAADKAVAGKAVHLMGLMSG 121
QY 125 GVSHHDHIFALIRAFKQLQVPKVFTHFPADGRDTSPTSGAGYLEQLLOFIASEKYGEIA 184
DB 122 GVSHEDHIYAAVEMAAAGAEEKIYLHCFLDGRDTPRSGAESLKRQDLFAKLKGRIA 181
QY 185 TITGRYYAMDRDRWERIRKWAYEPAIVGGIGQKATVDKAVDVVRERYAQSETDEFLPIYF 244
DB 182 SIYGRYYAMDRNDWRVEKAYDLLTLAGOE-FTYDSAVEALQAAAYAREENDEFVATEI 240
QY 245 SDQGR-----VKDDDTLIFENYRADRMQIC-----ECLGLERYKDLNSSLVPHKNIQISG 295
DB 241 RAQGQSAAMQDGDALLFMYRADRARQITRTVPDFAGFSR-----KAFP-----ALDFVM 292
QY 296 MTOYNKEFFPPSLFPVPTHNVLAELASQGVTFQFCAETEKYPHYVTFNFGNGREYQFQD 355
DB 293 LTQYAADIPLOCAFQASPLENTYGEWLSKAGKTQLRAISETEKYAHVTFNFGNGVENEFP 352
QY 356 EERCWVPSKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMNCNAPAPDMVGHGKTFEP 415
DB 353 EERQLVASPK-VATYDLOPEMSSKELTDKLVAASKGYDAITICNYPNGDMVGHGTVYEA 411
QY 416 AVKACQATDRAICKIFEACQTYNVLMVTSDHGNAEKMIAPD-GSEHTAHTCNLVPTCS 474
DB 412 AVKACEAVDCIGRVVEAIKEVDGQLLITADHGNAEMMIDPETGGVHTAHTSLPVPJ--- 468
QY 475 SKTFEYKSTPPTGDDGRARALRDVAPTVLQMLGLPVPPEMDG 518
DB 469 --IYGVNKAISLKEGK-----LSDLIAPTMLALSDLDIPADMSG 505

RESULT 9
AF0974
phosphoglycerate mutase (EC 5.4.2.1) - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
A:Note: this species has also been called Salmonella typhimurium
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0974
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Karpman, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, M.; S. J. Mouton, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Karpman, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, M.; S. J. Mouton, S.; O'Garra, P.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0974
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-507 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03290.1; PID:g16504911; GSPDB:GN00176
A:Gene: STY4091
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
C:Keywords: intramolecular transferase; isomerase

| | | | | |
|--|-----|-------------------------|---|---------|
| Qy | 68 | VGHUNIGAGRVIVODIVIRINLA | VORNEFVNPQIVASERAKKSGSRHLHLLGLVSDG | GVH 127 |
| Db | 59 | VGHVNLGAGRIVYQDLTRLDV | EEIKERITFANPVLITNAVDQAKNAGKAVHIMGLLSAG | GVH 118 |
| Qy | 128 | SHIDHFLAIRAFKQVPKV | FHFFADGRDTSPTSGAGVYQLQLQFIASEKYGELATIT | 187 |
| Db | 119 | SHEDHIWAWVELAAR | GAEKIYLHAFJLGRDTPPSRASELSUKFEDKFAALGKGRVASIV | 178 |
| Qy | 188 | GRYYARDRDKRWEIKMAY | EALVIGGIGQKATVDKAVDVVRERYASQSETDFELKPIVSDD | 247 |
| Db | 179 | GRYYARDRNRDRV | EKAYDLMTLAQGE-FQADTAVAGLAQAAYARDENFVKATVIRAE | 237 |
| Qy | 248 | GR-----VKDDTLTF | FFNYRADRMQICECL-----GLERYKDLNVSYPHPKNIQISGMT | 297 |
| Db | 238 | GQDAAMEEDGDTLTF | FMFRADRARREITRAFVNAFDGDFARKKVY-----NLNFVYLT | 289 |
| Qy | 298 | QYNKEFFPPSLFP | PVTHNLVLAEWLASOGVTFQFCAETEKYPHYTFPFNGGREVFQODEE | 357 |
| Db | 290 | EYAADITVAIYAP | PASLANTFGEWMKNDKQLRISETEKYAHVTFPFNGGVEEPPAGEE | 346 |
| Qy | 358 | RCMVPSPEVATYDLK | PEMNAAGVAEKVQIESGRHPLVMCNFPAPDMVGHHTGKFEPV | 417 |
| Db | 350 | RILLNSPK-VATYDLQ | PEMSSAELTEKLVAAIESKYDTIICNYPNGDMVGHTGVMEAAI | 408 |
| Qy | 418 | KACQATDEATGKIF | EACQTYNYVLMTVSDHNGNAEKMIAP-DGSHTAHTCNLVPFTCSSK | 476 |
| Db | 409 | KAVEALDNCIEQVT | KAVESVGGQLITADHGNABQMRDPATGOEHTAHTNLVPVL----- | 463 |
| Qy | 477 | TFVFKSTPTTGDG | CKERARALRDVAPTVLQMLGIPVPEMDGVPL | 521 |
| Db | 464 | IYGEKNVKA | VEGKK-----LSDIAPTMLSLMGWEIFQEMTGKPL | 503 |
| RESULT 10 | | | | |
| AG2328 | | | | |
| C:3-bisphosphoglycerate-independent phosphoglycerate mutase [imported] - Nostoc | | | | |
| C:Species: Nostoc sp. PCC 7120 | | | | |
| A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 | | | | |
| C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 | | | | |
| C:Accession: AG2328 | | | | |
| R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yanada, M.; Yasuda, M.; | | | | |
| DNA Res. 8, 205-213, 2001 | | | | |
| A:Title: Complete Genomic | | | | |
| A:Reference number: AB1807; MUID:21595285; PMID:11759840 | | | | |
| A:Accession: AG2328 | | | | |
| A:Status: preliminary | | | | |
| A:Molecule type: DNA | | | | |
| A:Residues: 1-533 <KUR> | | | | |
| A:Cross-references: GB:BA000019; PIDN:BAB75881.1; PID:g17133317; GSPDB:GN00179 | | | | |
| A:Experimental source: Strain PCC 7120 | | | | |
| C:Genetics: | | | | |
| A:Gene: all4182 | | | | |
| C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent | | | | |
| Query Match 38.7%; Score 1078; DB 2; Length 533; | | | | |
| Best Local Similarity 42.9%; Pred. No. 1.1e-78; | | | | |
| Matches 227; Conservative 85; Mismatches 179; Indels 38; Gaps 10; | | | | |
| Qy | 11 | VCLVVIDWGSLSD | HQHNAAKATPMDKLCSGNWQK-----LEAHGLHVLGPEGLMGN | 65 |
| Db | 9 | VVLVILDGWG | YEETRGNAIAAAKTPVMSL-----WTAYPHTLIHTSGKAVGLPEQGMGN | 64 |
| Qy | 66 | SEVGHNLNIGAGRV | IYQDITVRINLNAVORNEFVNPQIVASERAKKSGSRHLHLLGLVSDG | 125 |
| Db | 65 | SEVGHNLNIGAGRV | YQFVQLRIVSDAVDGSILNSALVKIQEVRNRNGKHLHVLGCSGG | 124 |
| Qy | 126 | VHSHDHLFALIRAF | KQLQVPKVTFHFADGRDTSPTSGAGVYQLQLQFIASEKYGELAT | 185 |
| Db | 125 | VHSHITHLFGLLDL | AEQRISEVCIHAITDGRDPTDGINAISALEDYINHVIGRIVT | 184 |
| Qy | 186 | ITGRYYAMDRDKR | WEIKMAYIV-GGIGQKATVDKAVDVVRERYASQSETDFELKPIV | 244 |

Db 185 VSGRYVAMDRRRVQRAYDVMTOGVGDGR---KAVDVLQASVAGVNDFFIVPVR 241
Qy 245 SDGRVKDDTLFFNYRADMRQIC-----ECLGLERYKOLNLSVPHPKNIQISQWTQ 298
Db 242 A-PGTVPGGVIFNFRPDRSRLQTAQAFVSPFTGARQQ-----IKPLSFTFTQ 292
Qy 299 YNKEFPFPPSVPTHTNVLAEWLASQGVTFQHCATEKYPHVTFNFGNGREVOFODEER 358
Db 293 YSDLSVSVAEPQNLNLTILGVIANOGLNQFRTAETEKYAHVTFYFNGGLEPFPAGEDR 352
Qy 359 CMVPSKEVATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPDMVGHGKFFPAVK 418
Db 353 ELVSSPM-VATYDKAPASATVDTAIAIQIGYISLVINIANPDMVGHGTOIEPTIK 411
Qy 419 ACQATDEAIGKIFACQTYNYVLMVTSDHGNAEKMIAPDGESEHTAHTCNVPPCTCSKTF 478
Db 412 AIVTDRCLGRLEGYSKAGGTWIIADHGNAEVYMLDEAGNSWTAHTNVPVLLIVEGK 471
Qy 479 V----FKSTPTPTGDKGERARALRDVAPTVLQMLGLPVPPMDGVPLLE 523
Db 472 VKIPGTYGTVNELRSDGK-----LADIAPTILDLQPPPEMTGRSLLQ 515

RESULT 11

AH0008

Phosphoglycerate mutase (EC 5.4.2.1) [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

C:Accession: AH0008

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AH0008

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-515 <R>

A:Cross-references: GB:AL590842; PIDN:CAC88930.1; PID:g15978177; GSPDB:GN00175

C:Genetics:

A:Gene: YPO0064

C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

C:Keywords: intramolecular transferase; isomerase

Query Match 38.5%; Score 1073.5; DB 2; Length 515;
Best Local Similarity 41.7%; Pred. No. 2.4e-78;
Matches 222; Conservative 95; Mismatches 176; Indels 39; Gaps 10;

Qy 6 NVQOKVCLVVDGWSLSDQHGNAIAKATPIMDKLCSGNWQK-----LEAHLHVGLPE 60
Db 3 STKKPLVLTLDGYGHREQODNAILNAKTPVMDVL----WQQPHTLIAASGLDVGLPD 58
Qy 61 GLMNGSEVHLNIGAGRIYQDITVRLNLAVEREFVNPQIVASAEKAKKSGRLHLGL 120
Db 59 GQMGNEVGHVNLGAGRIYQDITRUDKEIKEGDFNTNLTAAVDNAVTKCAVHIMGL 118
Qy 121 VSDGVVSHDHLFALIRAFKQLQVQKVIHFHFDAGDRTSPTSGAGLYLQQLQFASERY 180
Db 119 LSAGGVSHSHEDHIMAVELAAKRGATAIYLHAFLDGRTDPPRSAESSLRAKFAELGN 178
Qy 181 GELATITGRYAMDRKRERTKMAEYAVGGIGQKATVDKAVDVVRYRYAASETDFL 240
Db 179 GRIASIGRIYAMDRNRVQLAYDLTQARKE-FTADNAVAGLQAAYARGENDEFYK 237
Qy 241 PIVF-----SDQGRVKDDTLFFNYRADMRQI-----CECLGLERYKDLNLSVPHPKN 290
Db 238 PTVIQTGADAAWNEGDLTFNFRADRARQITRTFVNAEDFGKRAVWNG----- 291
Qy 291 IOISGMTQYNKEFPFSLFPVTHNVLAEWLASQGVTFQHCATEKYPHVTFNFGNGRE 350
Db 292 -DFIMLTEYAADIKVACAYPPASLTNTFCGLMKLHDKTQLRISETEKYAHVTFYNGVGE 350

Qy 351 VOFQDEERCWVSPKVEATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPDMVGH 410
Db 351 EPFKGEDRILINSPK-VATYDLQPEMSSAELTEKLSAIGSKYDVLICNYPNGDMVGH 409
Qy 411 GKFEPAVKACQATDEAIGKIFACQTYNYVLMVTSDHGNAEKMIAP-DGSEHTAHTCN 459
Db 410 GDYDAAVKAVETLQNCIEQVAAVKAADGQLLTADHGNAEQMRDPATGOAHTAHTSLPV 469
Qy 470 PFTCSKSTTVFKSTPTPTGDDGERARALRDVAPTVLQMLGLPVPPMDGVPL 521
Db 470 PL-----IYGNKAVKAVEGK-----LSDIAPTMLSLMEMEIPQEMTKPL 511

RESULT 12

F96987

2,3-bisphosphoglycerate-independent phosphoglycerate mutase gene [imported] - Clostridium

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001

C:Accession: F96987

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: F96987

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-510 <R>

A:Cross-references: GB:AE001437; PIDN:AAK78689.1; PID:g15023592; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0712

C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent

Query Match 38.2%; Score 1065; DB 2; Length 510;
Best Local Similarity 42.9%; Pred. No. 1.1e-77;
Matches 225; Conservative 99; Mismatches 176; Indels 24; Gaps 10;

Qy 8 QOKVCLVVDGWSLSDQHGNAIAKATPIMDKLCSGNW--OKLEAHLHVLGVLPEGLMGN 65
Db 3 KKPVMILMDGFGISDKVDGNVAKAASKPNEDKYFN-NYPHTHLGASGLSVGLPDQGMGN 61
Qy 66 SEVGHNLICAGRIYQDITVRLNLAVEREFVNPQIVASAEKAKKSGRLHLGLVSDGG 125
Db 62 SEVGHNLICAGRIYQSLTKITKATDGDGDFFRKALNKNVNVLENDSTLHLMGLLSPG 121
Qy 126 VHSHTDHLFALIRAFKQLQVQKVIHFHFDAGDRTSPTSGAGLYLQQLQFASERYGELAT 185
Db 122 VHSHTNHLKGLQLAKKKNVKKVFFHAFLDGDRDVPSSAKAFIKDIEDYVNEIGLGEIAT 181
Qy 186 ITGRYAMDRKRERIKMAYEAVGGIGQKATVDKAVDVVRYRYAQAQSETDFLKPIVES 245
Db 182 VSGRYAMDRNREREELAYNAMVLGKEEA--ESAIAKAVDASYHDNKTDFEVLPTVIV 239
Qy 246 DDGR-----VKDDTLFFNYRADMRQICECLGLERYKDLNLSVPHPKNIQISGMTQYNK 301
Db 240 KEKGPVATIKDSDVIFNFRDPRARQITRAAEAFDGFKR-----RLNIEFVMTVEYDA 296
Qy 302 EPPFSL-FPPVTHNVLAEWLASQGVTFQHCATEKYPHVTFNFGNGREVOFQDERCM 360
Db 297 SFKGVDAFAGPENINTLGEYVSNKGLNQLRTAETEKYAHVTFNFGNGVEEENKNDRLAL 356
Qy 361 VSPKVEATYDLKPEMNAAGVAEKVQIESGRHPLVMCNFAPDMVGHGKFFPAVKAC 420
Db 357 ISSPK-VATYDLKPEMSAVETDELKRLDEDDKYDMVILNANFANPDMVGHGTLAEAKKAV 415
Qy 421 QATDEAIGKIFACQTYNYVLMVTSDHGNAEKMI-APDGESEHTAHTCNVLPPTCSKTFV 479
Db 416 ETVDECLKIVDKVLKLDGSEVITADHGNSEQIMIDYSGNKPMTAHTVNPVPF-----YVV 470
Qy 480 FKSTPTPTGDKGERARALRDVAPTVLQMLGLPVPPMDGVPLLE 523
Db 471 SNHT-----EAKNLNGLVADIAPTMLQEMGLEKPEMTGKSLFE 510

RESULT 13

S47833
Probable phosphoglycerate mutase (EC 5.4.2.1), 2,3-diphosphoglycerate-independent - Esch
N:Alternate names: hypothetical protein o514
C:Species: Escherichia coli
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 01-Mar-2002
C:Accession: S47833; F65161
R:Plunkett, G
Submitted to the EMBL Data Library, March 1994
A:Reference number: S47666
A:Accession: S47833
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-514 <PLU>
A:Cross-references: EMBL:U00039; NID:9466582; PIDN:AA818599.1; PID:9466750
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F65161
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-514 <BLAT>
A:Cross-references: GB:AE000439; GB:U00096; NID:q1790036; PIDN:AAC76636.1; PID:q1790041.
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: y1b0
C:Superfamily: phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
C:Keywords: intramolecular transferase; isomerase

Query Match 38.2%; Score 1063; DB 2; Length 514;
Best Local Similarity 41.1%; Pred. No. 1.7e-77;
Matches 218; Conservative 99; Mismatches 173; Indels 40; Gaps 10;

```
Qy 8 QQKVCVVIDGWLSDQHGNAIAKAKTPIMDKLCSGNWQK-----LEAHGLHVGLPEGL 62
Db 5 KKPWVLVDGYYREQODNAIFSAKTPVMDAL----WANRPHTLIDASGLEVLGPDQR 60

Qy 63 MGSEVGHNLGAGRIYQDVRINLAVQRNEFTNPOIVASAEARAKKSGRLHLLGLVS 122
Db 61 MGSEVGHNLGAGRIYQDVRINLAVQRNEFTNPOIVASAEARAKKSGRLHLLGLVS 120

Qy 123 DGGVSHDHFLALIRAFKQLQVPKVFTHFPADGRDTPSPGAGYLEQLQFIASEKYGE 182
Db 61 MGSEVGHNLGAGRIYQDVRINLAVQRNEFTNPOIVASAEARAKKSGRLHLLGLVS 120

Qy 123 DGGVSHDHFLALIRAFKQLQVPKVFTHFPADGRDTPSPGAGYLEQLQFIASEKYGE 182
Db 121 AGGVSHEDHIMAVELAAERGAEKIYLHAFDGRDTPSPGAGYLEQLQFIASEKYGE 180

Qy 183 LATITGRYAMDROKRWERIKMAYEIVGGIGQKATVDKAVDVVRYRYAQSDEFLKPI 242
Db 181 VASIIIGRYAMDROKRWERIKMAYEIVGGIGQKATVDKAVDVVRYRYAQSDEFLKPI 242

Qy 243 VFSDDGR-----VKDDDTLIFNYRADRMQICECL-----GLERYKDLNSSLVPHPKNIQ 292
Db 240 VIRAEQPDAAEMDGDALIFMNFRAAREITRAFVNAEDFGFARKVW-----NVD 291

Qy 293 ISGMTQYNKEPFPSPFPVTHTNVLAELASQGVTFQHCATEKYPHVTFFNGGREVQ 352
Db 292 FVMLTEYAADIKTAVAYPPASLVNTFGEWMAKNKDTQLRISETEKYAHVTFFFNGGVEES 351

Qy 353 FQDERCMVPSKPVATYDLKPEMNAAGVAKMVEQIESGRHPLVMCNFAPDPMVGHTGK 412
Db 352 FKGEDRLILNSPK-VATYDLQPEMSSAELTEKLVAAIKSGKYDIIICNYPNGDMVGHTGV 410

Qy 413 FEPVAKCAQATDEAIGKIFEACQYNNVYLVMTSDHNAEKMIAP-DGSEHTAHTCNLVPF 471
Db 411 MEAAVKAVALDHCVAEVAKAVESVGGQLLITADHNAEQMRDPATGQAHTAHTNLPVPL 470

Qy 472 TCSSKTFVFKSTPTPTGDDGERARALRDVATVTLQMLGLPVPPEMDGVPL 521
Db 471 -----IYVGDKNKVAVEGGK-----LSDIAPTMLSLMGMEIPQEMTKPL 510
```

RESULT 15

C86037
hypothetical protein y1b0 [imported] - Escherichia coli (strain O157:H7, substrain ED
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C86037
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

Search completed: July 31, 2003, 13:35:35
Job time : 43 secs

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Job time : 43 secs